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1 / 32

Figure 1

M K H L W F F L L L V A A P R
GAC ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA

+1 10
W V L S Q V Q L Q E A G P G L V
TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG

20
K P S E T L S L T C S V S G G S
AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC

30 40
I S G D Y Y W F W I R Q S P G K
ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG

50 60
G L E W I G Y I Y G S G G G T N
GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT

70
Y N P S L N N R V S I S I D T S
TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC

80 90
K N L F S L K L R S V T A A D T
AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG

100
A V Y Y C A S N I L K Y L H W L
GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA

110 120
L Y W G Q G V L V T S S
TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC



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2 / 32

Figure 2

M A W A L L L L G L L A H F T
ACC ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA

+1 10
D S A A S Y E L S Q P R S V S V
GAC TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG

20
S P G Q T A G F T C G G D N V G
TCC CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA

30 40
R K S V Q W Y Q Q K P P Q A P V
AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG

50 60
L V I Y A D S E R P S G I P A R
CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA

70
F S G S N S G N T A T L T I S G
TTC TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG

80 90
V E A G D E A D Y Y C Q V W D S
GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT

100
T A D H W V F G G G T R L T V L
ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA

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3 / 32
Figure 3

Frame 1 Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp Ser Ala Ala
ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA GAC TCT GCG GCC
9 18 27 36 45 54

Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser Pro Gly Gln Thr Ala Gly Phe Thr
TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG TCC CCA GGA CAG ACG GCC GGG TTC ACC
66 75 84 93 102 111 120

Cys Gly Gly Asp Asn Val Gly Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala
TGT GGG GGA GAC AAC GTT GGA AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC
129 138 147 156 165 174 183

Pro Val Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe Ser Gly
CCT GTG CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA TTC TCT GGC
192 201 210 219 228 237 246

Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val Glu Ala Gly Asp Glu Ala Asp
TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG GTC GAG GCC GGG GAT GAG GCT GAC
255 264 273 282 291 300 309

Tyr Tyr Cys Gln Val Trp Asp Ser Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu
TAT TAC TGT CAG GTG TGG GAC AGT ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CCG CTG
318 327 336 345 354 363 372

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
ACC GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG
381 390 399 408 417 426 435

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG ACA
444 453 462 471 480 489 498

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys
GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA
507 516 525 534 543 552 561

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC
570 579 588 597 606 615 624

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT
633 642 651 660 669 678 687

Thr Glu Cys Ser TER
ACA GAA TGT TCA TGA



Appln. No.: 09/612,914
INVENTOR: Nabli HANNA et al.
FILED: July 10, 2000
ATTORNEY DOCKET: 037003/0275643
IDEC REF. NO.: 1999-30-0019CP4C1
TITLE: RECOMBINANT ANTI-CD4 ANTIBODIES OR HUMAN THERAPY
PILLSBURY WINTHROP LLP
MCLEAN, VIRGINIA

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4 / 32
Figure 4a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
ATG AAA CAC CTG TGG TTC TTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAC CTC TTC TCC CTG AAA CTG
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGC
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Ser Glu Ser Thr Ala Ala Leu Gly
CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC
507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro

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5 / 32

Figure 4 b

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC CCA
696 705 714 723 732 741 750

Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
GCA	CCT	GAG	TTC	CTG	GGG	GGA	CCA	TCA	GTC	TTC	CTG	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACT	CTC
		759			768			777			786			795			804			813

Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC	GAG
		822			831			840			849			858			867			876

Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
GTC	CAG	TTC	AAC	TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG
		885			894			903		912				921			930			939

Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Tyr	Leu
GAG	CAG	TTC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG
		948			957			966		975				984			993			1002

Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
AAC	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GGC	CTC	CCG	TCC	TCC	ATC	GAG	AAA	ACC
1011			1020			1029			1038			1047			1056			1065		

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG
1074 1083 1092 1101 1110 1119 1128

Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
GAG	ATG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAC	CCC	AGC	GAC	ATC
	1137				1146			1155			1164			1173			1182			1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG
1200 1209 1218 1227 1236 1245 1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG
1263 1272 1281 1290 1299 1308 1317

Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
GGG	AAT	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACA	CAG	AAG	AGC
	1326			1335				1344			1353			1362			1371			1380

Leu Ser Leu Ser Leu Gly Lys TER
CTC TCC CTG TCT CTG GGT AAA TGA
1389 1398



Appl. No.: 09/612,914
INVENTOR: Nabil HANNA et al.
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6 / 32

Figure 5a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC
507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro

7 / 32

Figure 5 b

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC CCA
696 705 714 723 732 741 750

Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
GCA	CCT	GAG	TTC	GAG	GGG	GGA	CCA	TCA	GTC	TTC	CTG	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACT	CTC
		759			768			777			786			795			804			813

Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC	GAG
		822			831			840				849		858			867			876

Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
GTC	CAG	TTC	AAC	TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG
		885			894			903			912			921			930			939

Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
GAG	CAG	TTC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG
		948			957			966			975			984			993			1002

Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
AAC	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GGC	CTC	CCG	TCC	TCC	ATC	GAG	AAA	ACC
1011			1020			1029			1038			1047			1056			1065		

Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CAG	GAG
	1074			1083				1092			1101			1110			1119			1128

Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile		
GAG	ATG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAC	CCC	AGC	GAC	ATC		
			1137			1146			1155			1164			1173			1182			1191	

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG
1200 1209 1218 1227 1236 1245 1254

Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AGG	CTA	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	GAG
		1263			1272			1281			1290			1299			1308			1317

Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
GGG	AAT	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACA	CAG	AAG	AGC
	1326				1335			1344			1353			1362		1371			1380	

Leu Ser Leu Ser Leu Gly Lys TER
CTC TCC CTG TCT CTG GGT AAA TGA
1389 1398

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8 / 32

Figure 6a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC
507 516 525 534 543 552 561

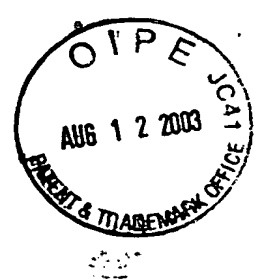
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro

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10 / 32

Figure 7a

Primers for the Amplification of Monkey Immunoglobulin Heavy Chain Variable Regions

5' 'Sense' Primers

A. Human or Monkey heavy chain early leader sequence primers with *Sall* site

- V_H1 5' ACTAAGTCGACATGGACTGGACCTGG 3'
V_H2 5' ACTAAGTCGACATGGACATACTTTGTTCCAC 3'
V_H3 5' ACTAAGTCGACATGGAGTTTGGGCTGAGC 3'
V_H4 5' ACTAAGTCGACATGAAACACCTGTGGTTCTT 3'
V_H5 5' ACTAAGTCGACATGGGGTCAACCGCCATCCT 3'
V_H6 5' ACTAAGTCGACATGTCTGTCTCCTTCCTCAT 3'

B. Human or Monkey heavy chain late leader sequence primers with *Mlu* I site

- V_H1 5' G GCA GCA GC(CT) ACG CGT GCC CAC TCC GAG GT 3'
V_H2 5' G ACC GTC CCG ACG CGT GT(TC) TTG TCC CAG GT 3'
V_H3 5' GCT ATT TTC ACG CGT GTC CAG TGT GAG 3'
V_H4 5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3'
V_H5 5' G GCT GTT CTC ACG CGT GTC TGT GCC GAG GT 3'



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TITLE: RECOMBINANT ANTI-CD4 ANTIBODIES OR HUMAN THERAPY

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11 / 32

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Figure 7b

C. Human or Monkey framework 1 sequence primers with *Xho* I site

V _H 1,3a,5	+1 CAGGTGCAGCTGCTCGAGTCTGG
V _H 2	+1 CAGGTCAACTTACTCGAGTCTGG
V _H 3b	+1 GAGGTGCAGCTGCTCGAGTCTGG
V _H 4	+1 CAGGTGCAGCTGCTCGAGTCGGG
V _H 6	+1 CAGGTACAGCTGCTCGAGTCAGG

3' 'Anti-Sense' Primers.

A. Human or Monkey Heavy Chain Constant Region Primers Anti-Sense Strand with *Nhe* I site

IgG ₁₋₄	+118	5' GGC GGA TGC GCT AGC TGA GGA GAC GG 3'	+110
		Nhe I	



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Figure 7c

Primers for the Amplification of Monkey Immunoglobulin Light Chain Variable Regions

5' 'Sense' Primers

A. Human or Monkey kappa light chain early leader primers with Bgl II site

1. 5' ATCACAGATCTCTCACCATGGTGTTCAGACCCAGGTC 3'
2. 5' ATCACAGATCTCTCACCATGG(GA)G(AT)CCCC(TA)GC(TG)CAGCT 3'
3. 5' ATCACAGATCTCTCACCATGGACATGAGGGTCCCCGCTCAG 3'
4. 5' ATCACAGATCTCTCACCATGGACAC(GAC)AGGGCCCCCACTCAG 3'

B. Human or Monkey lambda light chain early leader primers with Bgl II site

1. 5' ATCACAGATCTCTCACCATGGCCTGGGCTCTGCTGCTCC 3'
2. 5' ATCACAGATCTCTCACCATGGCCTGGGCTCCACTACTTC 3'
3. 5' ATCACAGATCTCTCACCATGACCTGCTCCCCTCTCCTCC 3'
4. 5' ATCACAGATCTCTCACCATGGCCTGGACTCCTCTCTTTC 3'
5. 5' ATCACAGATCTCTCACCATGACTTGGACCCCACTCCTC 3'

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Figure 8

A. Heavy Chain Variable Region:

VH1	5'	CCATGGACTGGACCTGG	3'
VH2	5'	ATGGACATACTTTGTTCCAC	3'
VH3	5'	CCATGGAGTTTGGGCTGAGC	3'
VH4	5'	ATGAAACACCTGTGGTTCTT	3'
VH5	5'	ATGGGGTCAACCGCCATCCT	3'
VH6	5'	ATGTCTGTCTCCTTCCTCAT	3'

B. Heavy Chain Constant Region Anti-Sense Strand:

IgM	5'	⁺¹¹⁹ T TGG GGC GGA TGC ACT	⁺¹¹⁵ 3'
IgG ₁₋₄	5'	⁺¹¹⁹ GA TGG GCC CTT GGT GGA	⁺¹¹⁵ 3'

C. Light Chain Variable Region:

Kappa	5'	⁺⁴ G ATG ACC CAG TCT CCA (G/T)CC TC	⁺¹⁰ 3'
Lambda	5'	⁻⁹ CTC A(C/T)T (T/C)(G/A)C TGC (A/C)CA GGG TCC	⁻³ 3'

D. Light Chain Constant Region Anti-Sense Strands:

Kappa	5'	⁺¹¹⁵ AA GAC AGA TGG TGC AGC CA	⁺¹¹⁰ 3'
Lambda	5'	⁺¹¹⁸ G GAA CAG AGT GAC CGA GGG G	⁺¹¹² 3'



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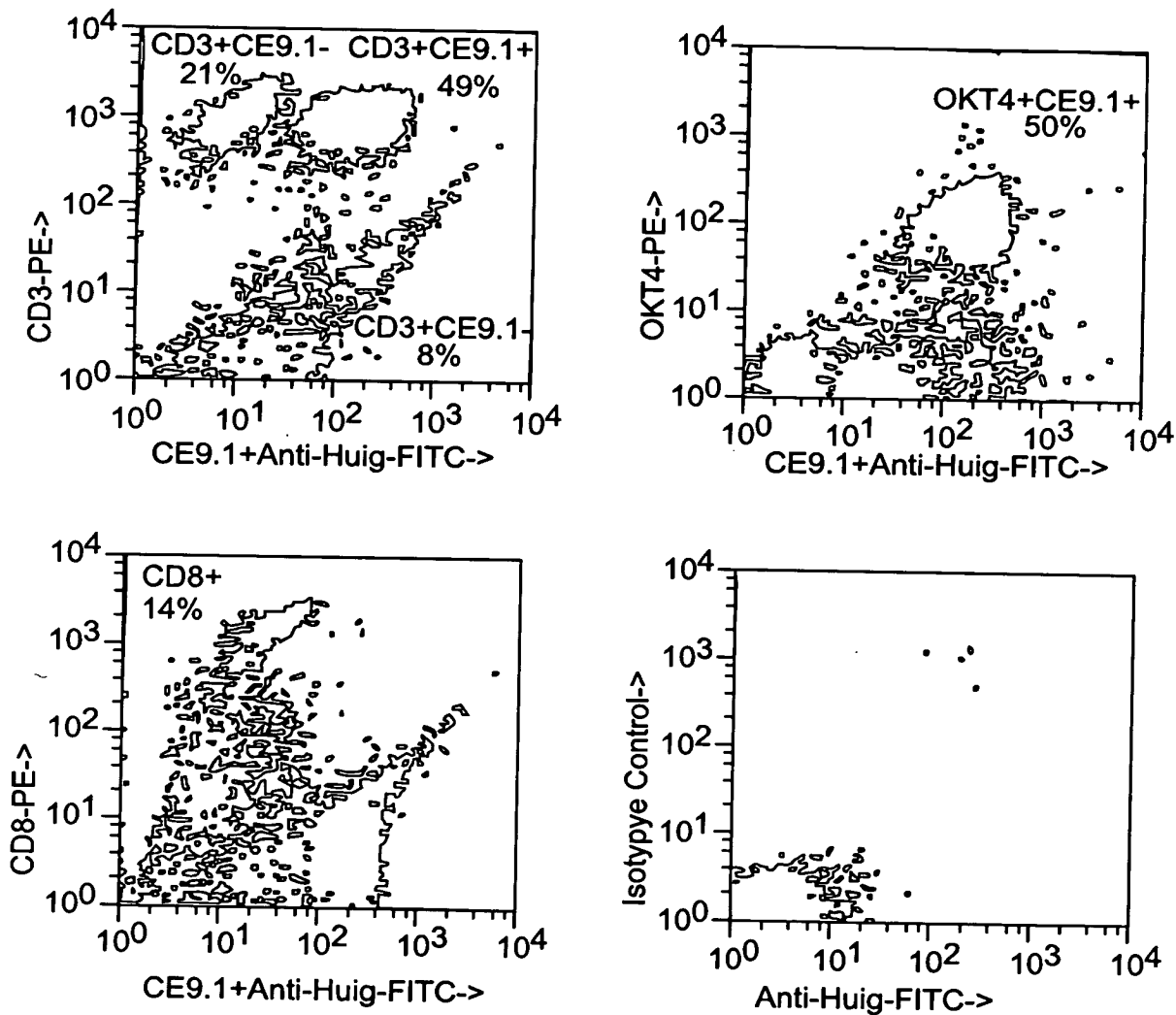


Figure 9



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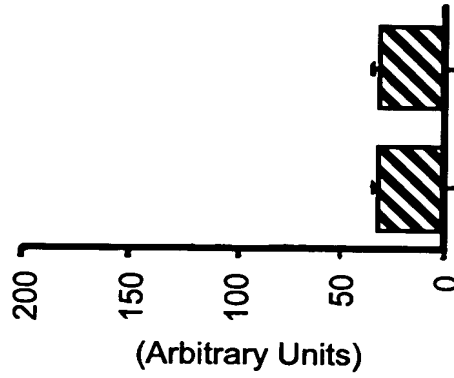


Figure 10c

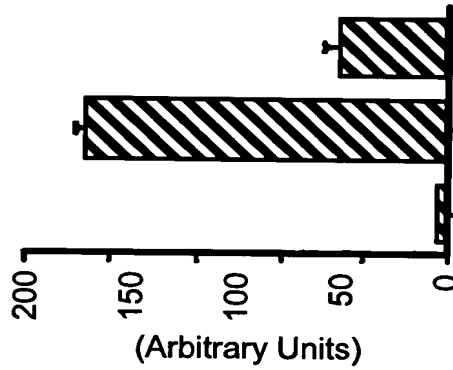


Figure 10b

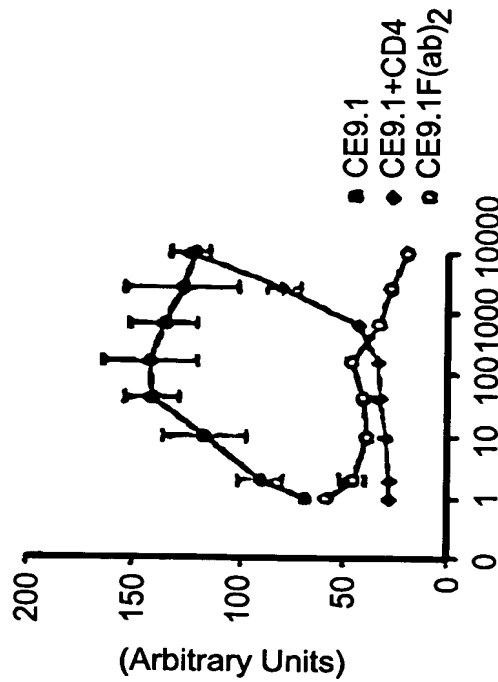


Figure 10a



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17 / 32

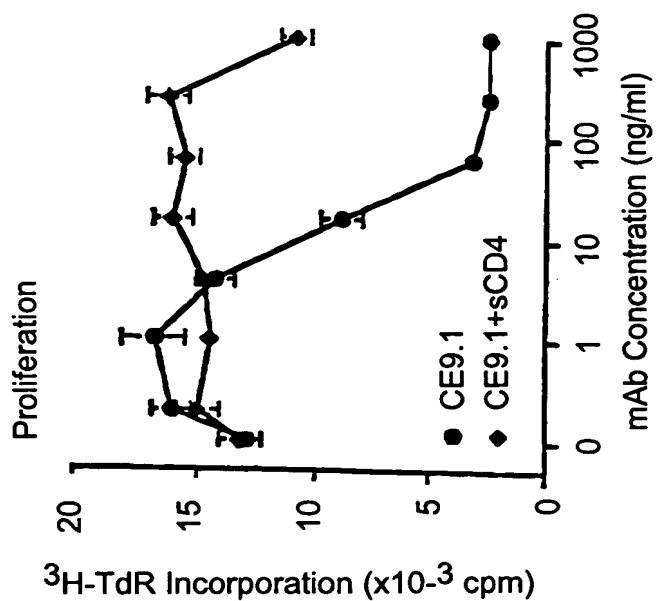
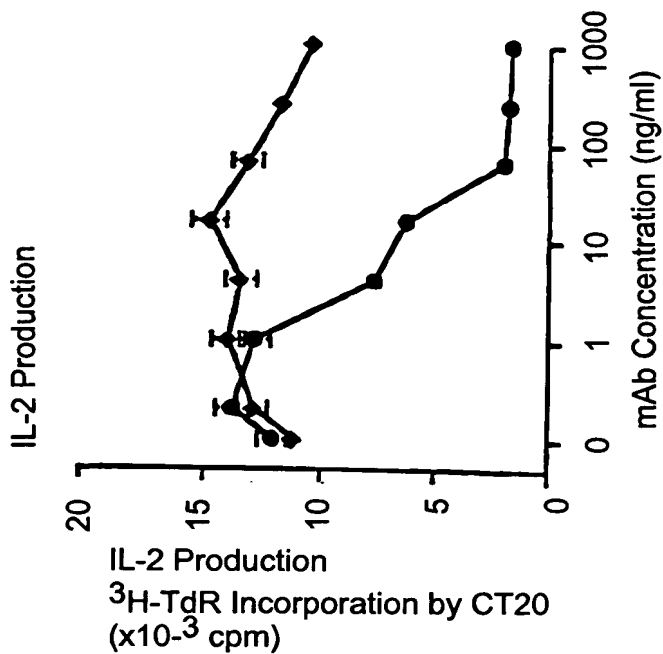


Figure 11



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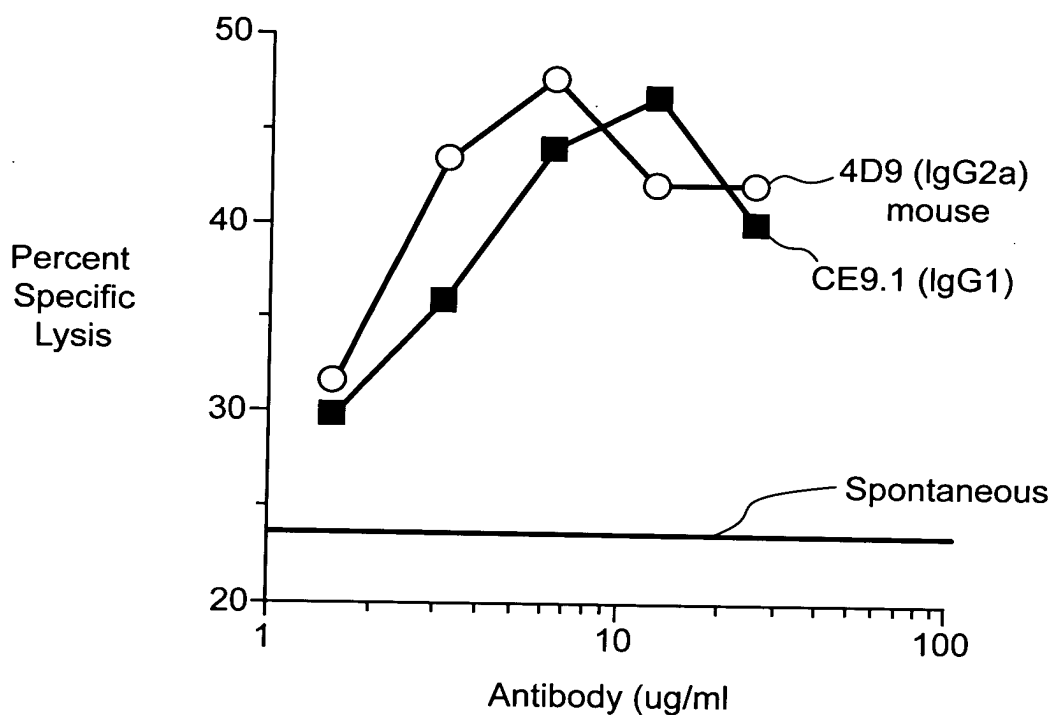


Figure 12



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INVENTOR: Nabli HANNA et al.
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ATTORNEY DOCKET: 037003/0276643
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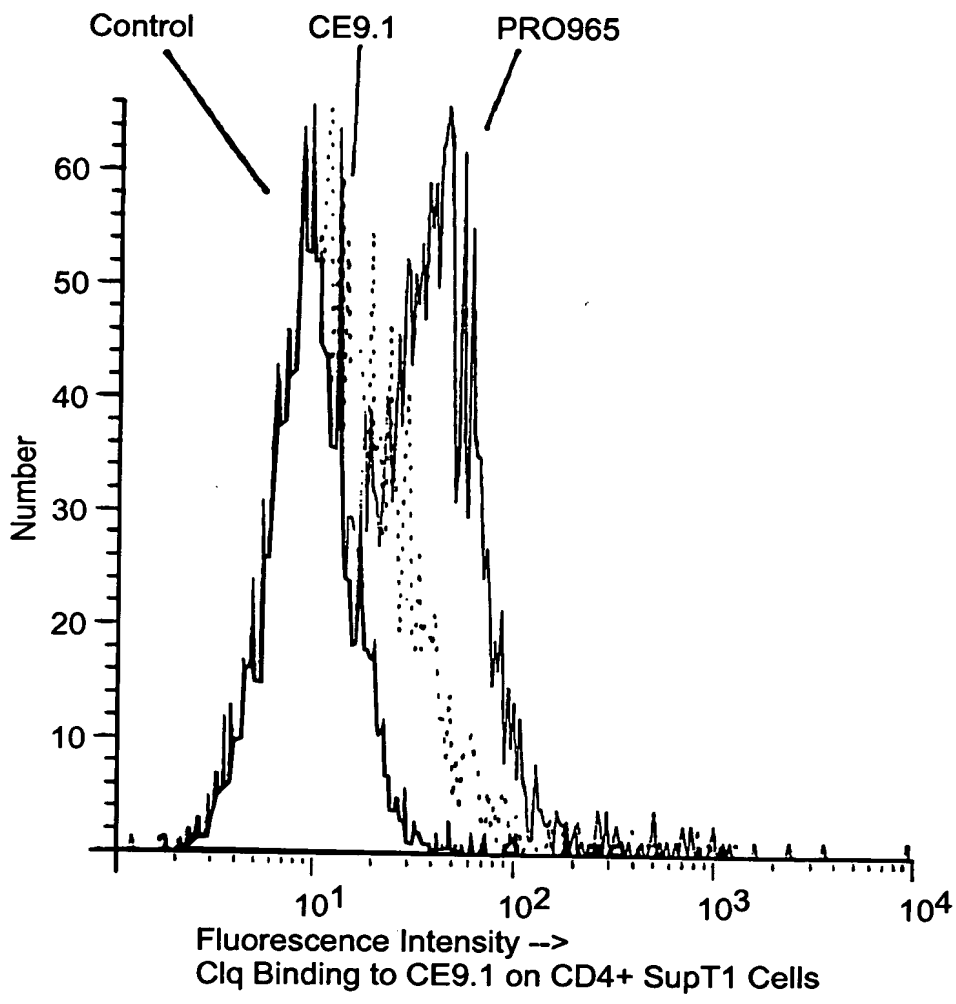


Figure 13



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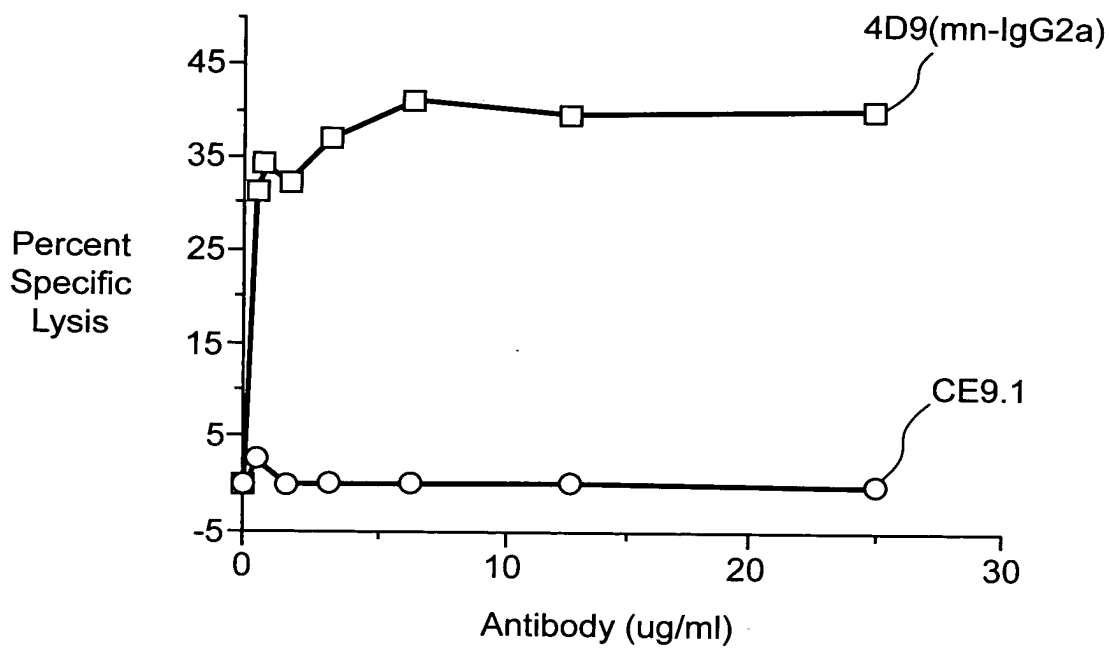


Figure 14

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Figure 16

PCR Primers for Human $\gamma 4$ Constant Region

1) IDEC 462 3' PCR Primer
5' GGGG GGA TCC TCA TTT ACC CAG AGA CAG GG 3'
BamH I

2) IDEC 479 5' PCR Primer
5' GGGG GCT AGC ACC AAG GGC CCA TCC GTC TTC 3'
Nhe I

PCR Mutagenesis of Human $\gamma 4$

3) IDEC 698 3' PCR Primer
5' CCG GGA GAT CAT GAG AGT GTC CTT GGG TTT TGG GGG GAA CAG GAA GAC
BspH I

TGA TGG TCC CCC CTC GAA CTC AGG TGC TGG GCA TGG TGG GCA TGG GGG 3'
Glu Pro

4) Midland GE212 5' PCR Primer

5' TCC TCA GCT AGC ACC AAG GGG CCA TCC 3'
Nhe I
Destroys Apa I site



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Figure 17a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC
9 18 27 36 45 54

+1
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
66 75 84 93 102 111 120

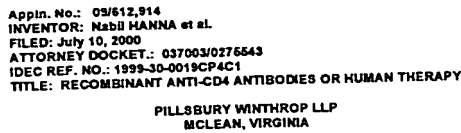
Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG
381 390 399 408 417 426 435



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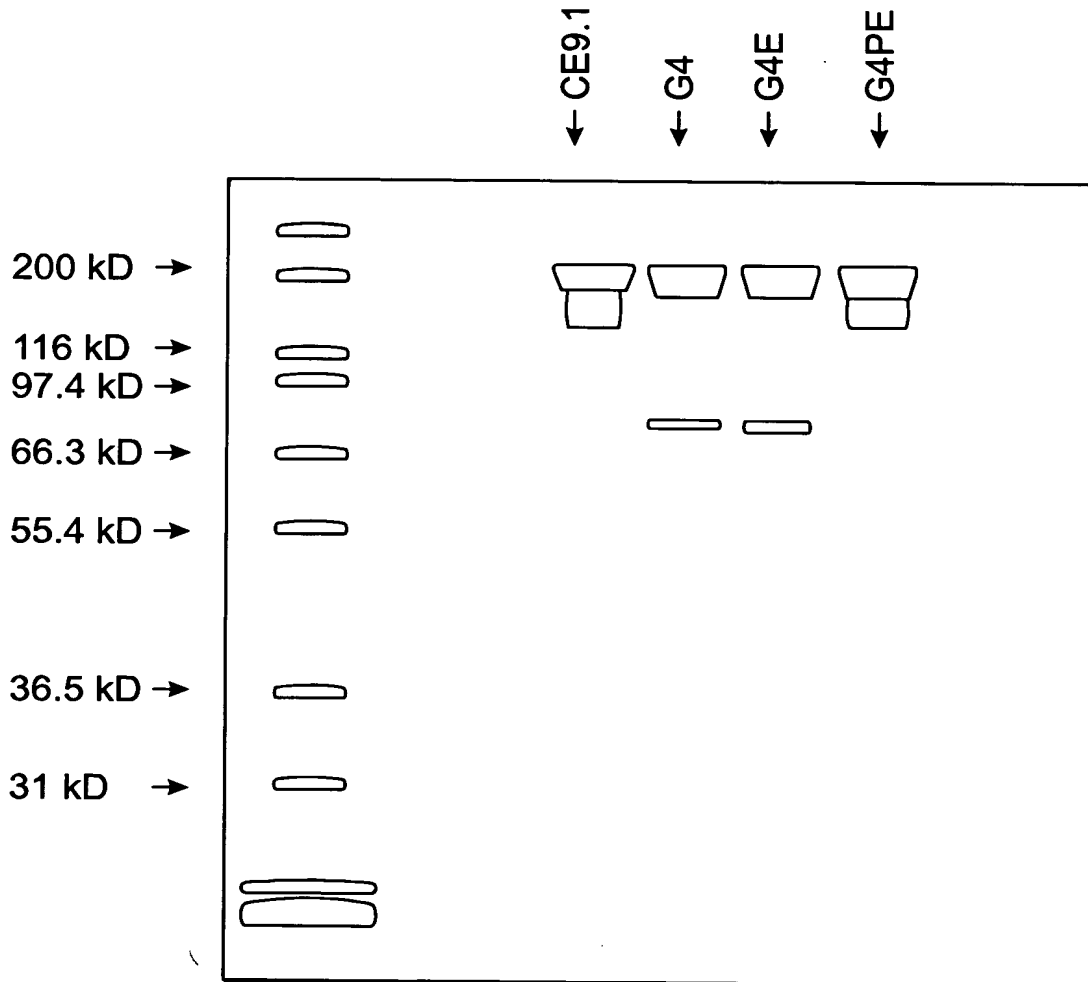


Figure 18

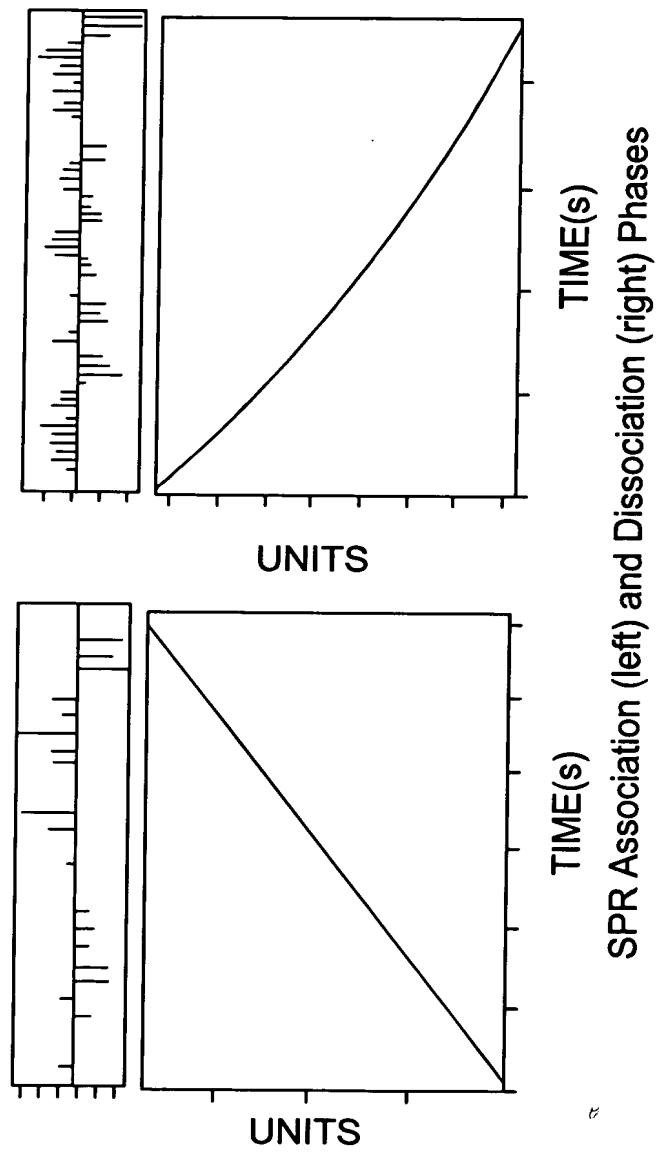


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FILED: July 10, 2000
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Figure 19

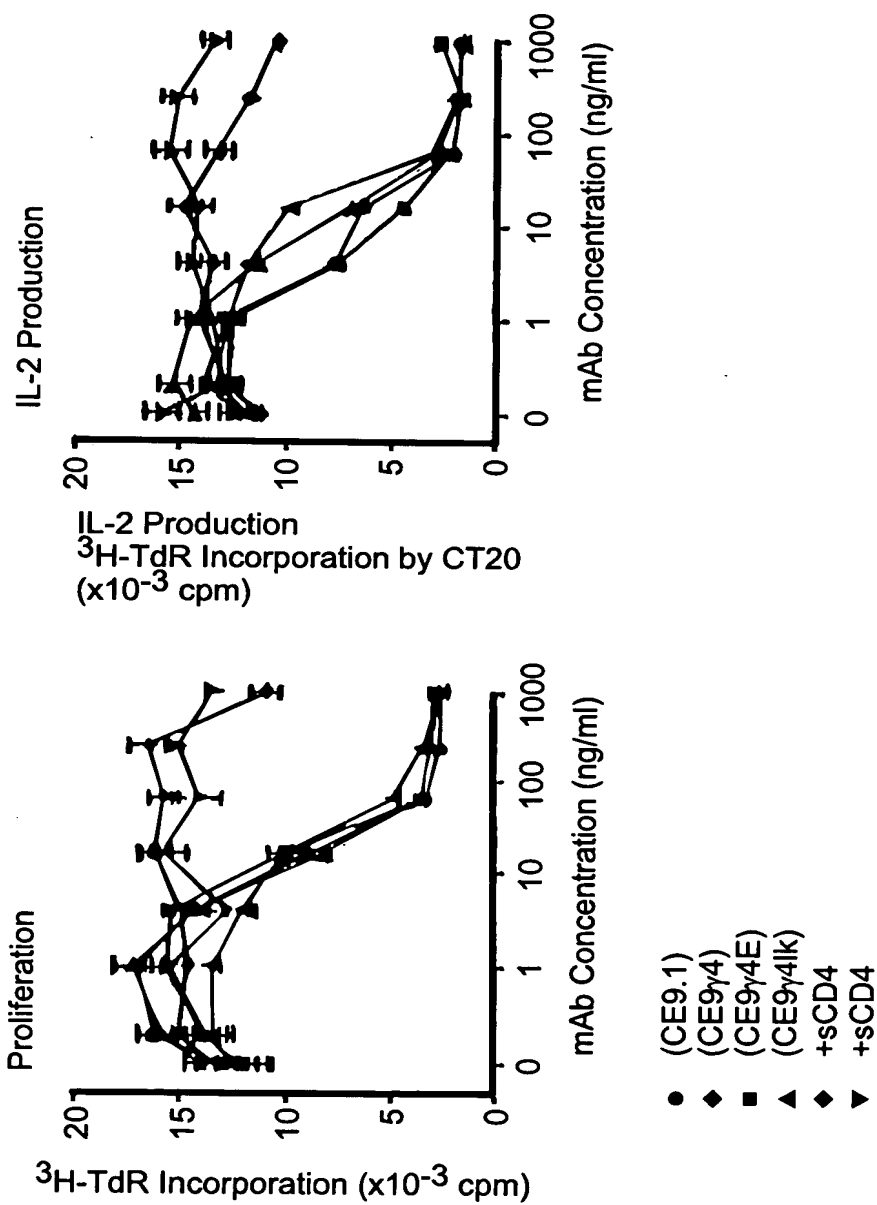




27 / 32

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Figure 20



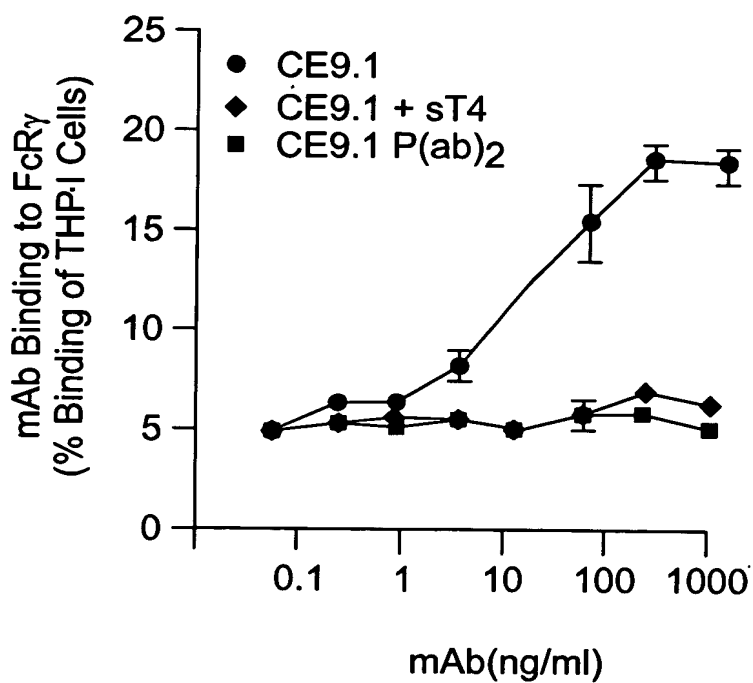


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Figure 21

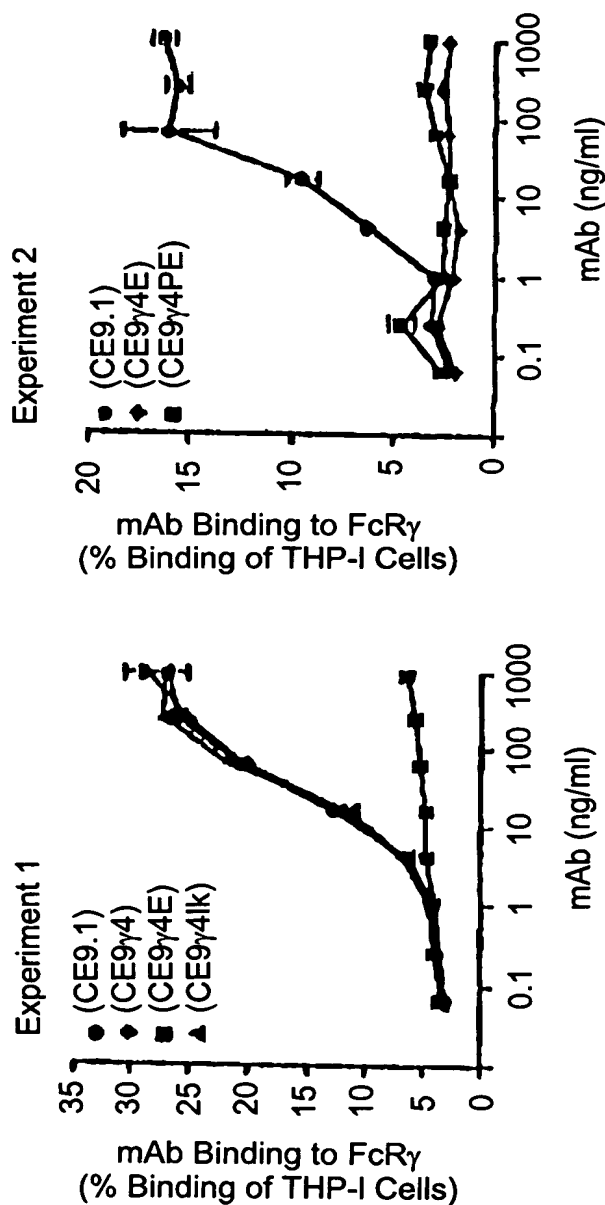




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Figure 22





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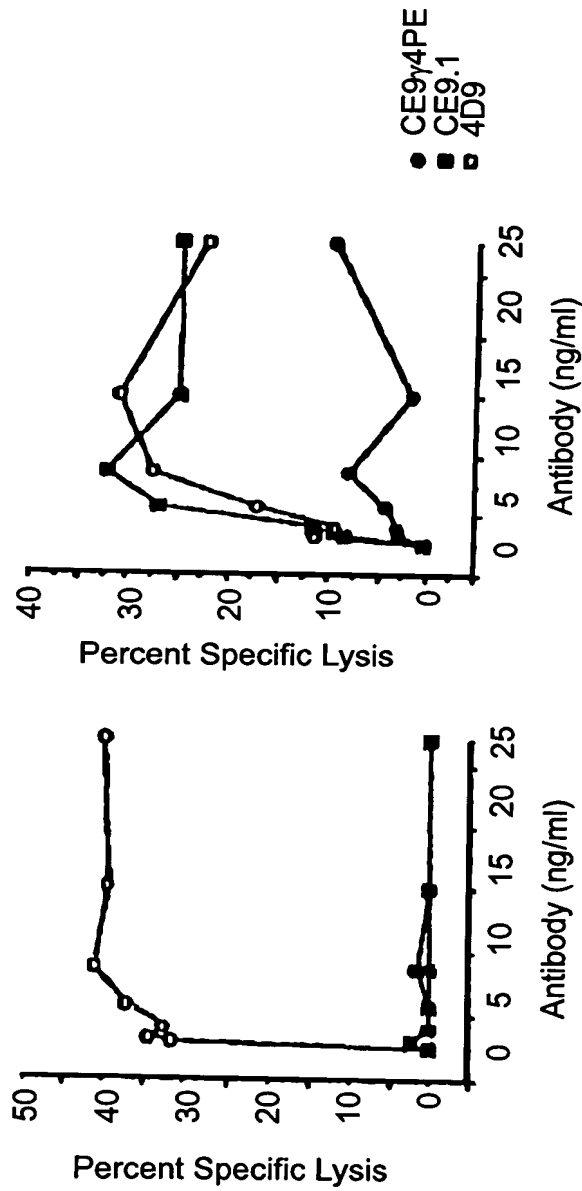
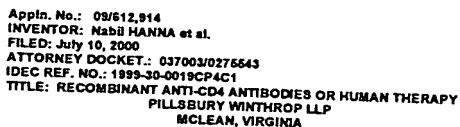


Figure 23



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Figure 1 is a semi-logarithmic plot showing the plasma concentration (ug/ml) versus time (Hour) for eight rats. The y-axis is logarithmic, ranging from 0.01 to 100 ug/ml. The x-axis is linear, ranging from 0 to 700 hours. The legend indicates eight data series: E, rat # 15 (open square), E, rat # 16 (open triangle), E, rat # 17 (asterisk), E, rat # 18 (open circle), PE, rat # 13 (open square), PE, rat # 14 (open circle), PE, rat # 19 (open circle), and PE, rat # 20 (open triangle). The E series generally show higher concentrations and slower elimination compared to the PE series.



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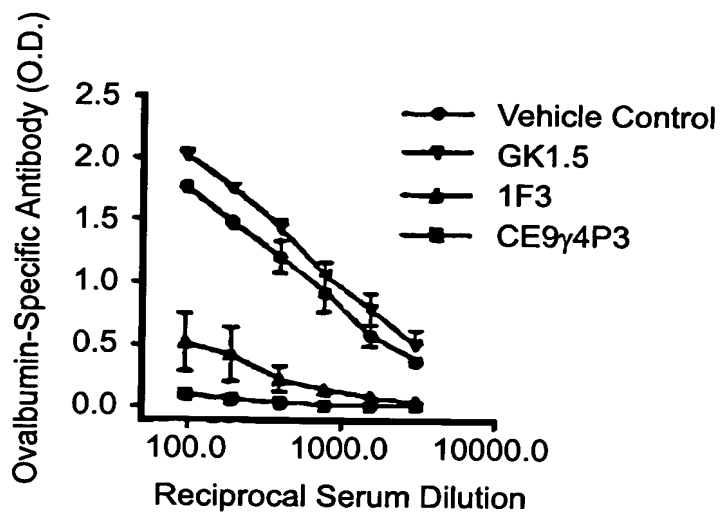


Figure 25